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RAW SEQUENCE LISTING

DATE: 02/19/2002

PATENT APPLICATION: US/10/058,945

TIME: 11:02:15

Input Set : A:\215482US0X.txt

Output Set : N:\CRF3\02192002\J058945.raw

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3 <110> APPLICANT: HERMANN, Thomas
4      WOLF, Andreas
5      MORBACH, Susanne
6      KRAMER, Reinhard
8 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE OtsA PROTEIN
10 <130> FILE REFERENCE: 215482US0X
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/058,945
C--> 12 <141> CURRENT FILING DATE: 2002-01-30
12 <150> PRIOR APPLICATION NUMBER: DE 10103873.9
13 <151> PRIOR FILING DATE: 2001-01-30
15 <150> PRIOR APPLICATION NUMBER: DE 10110760.9
16 <151> PRIOR FILING DATE: 2000-03-07
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3010
24 <212> TYPE: DNA
25 <213> ORGANISM: Corynebacterium glutamicum
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (884)..(2338)
30 <223> OTHER INFORMATION:
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36 ggccccgtct ctgccgctgc gattgctgca acagcagttg gtttcaactgg tggtttgctt      120
38 gcccgctgat tcttgattcc accggttgatt gtggcgattg ccggcatcac accaatgctt      180
40 ccagggtctag caatttaccg cgggaatgtac gccacctga atgatcaaac actcatgggt      240
42 ttcaccaaca ttgcggttgc tttagccact gtttcatcac ttgccgctgg cgtggttttg      300
44 ggtgagtgga ttgccgcgag gctacgtcgt ccaccacgct tcaacccata ccgtgcattt      360
46 accaaggcga atgagttctc cttccaggag gaagctgagc agaatcagcg ccggcagaga      420
48 aaacgtccaa agactaatca gagattcggg aataaaaagg aaaaatcaac ctgcttaggc      480
50 gtcttttcgt taaatagcgt agaatacgg gtcgatcgt tttaaacact caggaggatc      540
52 cttgccggcc aaaatcacgg acactcgtcc caccacagaa tcccttcacg ctgttgaaaga      600
54 ggaaaccgca gccgggtgcc gcaggattgt tgccacctat tctaaggact tcttcgacgg      660
56 cgtcactttg atgtgcatgc tcggcggtga acctcagggc ctgcgttaca ccaaggctgc      720
58 ttctgaacac gaggaagctc agccaaagaa ggctacaaag cggactcgta aggcaccagc      780
60 taagaaggct gctgctaaga aaacgaccaa gaagaccact aagaaaacta ctaaaaagac      840
62 caccgcaaag aagaccacaa agaagtctta agccgatct tat atg gat gat tcc      895
63                                     Met Asp Asp Ser
64                                     1
66 aat agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc      943
67 Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val
68 5              10              15              20

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70 cac cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc      991
71 His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val
72          25          30          35
74 acg ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga      1039
75 Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly
76          40          45          50
78 tgg cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg      1087
79 Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr
80          55          60          65
82 ggt gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc      1135
83 Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly
84          70          75          80
86 ttc tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat      1183
87 Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp
88 85          90          95          100
90 ctg att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg      1231
91 Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg
92          105          110          115
94 gag gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac      1279
95 Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His
96          120          125          130
98 ggt gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc      1327
99 Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Val Pro Gly
100          135          140          145
102 att ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac      1375
103 Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His
104          150          155          160
106 att ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa      1423
107 Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu
108 165          170          175          180
110 gag att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg      1471
111 Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu
112          185          190          195
114 gtt caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc      1519
115 Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly
116          200          205          210
118 act gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt      1567
119 Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly
120          215          220          225
122 gaa gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga      1615
123 Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly
124          230          235          240
126 agg cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg      1663
127 Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met
128 245          250          255          260
130 ttt ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc      1711
131 Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu
132          265          270          275
134 gac gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc      1759

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135 Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr
136          280          285          290
138 aag ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc      1807
139 Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser
140          295          300          305
142 ggc gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct      1855
143 Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro
144          310          315          320
146 tcg cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag      1903
147 Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu
148 325          330          335          340
150 gaa gcc gtc gcc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc      1951
151 Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro
152          345          350          355
154 gtg gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg      1999
155 Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val
156          360          365          370
158 ctg tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt      2047
159 Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly
160          375          380          385
162 atg aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act      2095
163 Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr
164          390          395          400
166 ggt gct ttg gtg ctg tcc gaa ttt gcc gcc gcg gcc act gag ctg acc      2143
167 Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr
168 405          410          415          420
170 ggt gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa      2191
171 Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln
172          425          430          435
174 atg gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca      2239
175 Met Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala
176          440          445          450
178 acg cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac      2287
179 Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn
180          455          460          465
182 gtg tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac      2335
183 Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn
184          470          475          480
186 tca tgaaccgcgc acgaatcgcg accataggcg ttcttccgct tgctttactg      2388
187 Ser
188 485
190 ctggcgctct gtggttcaga caccgtggaa atgacagatt ccacctgggt ggtgaccaat      2448
192 atttacaccg atccagatga gtcgaattcg atcagtaatc ttgtcatttc ccagcccagc      2508
194 ttagattttg gcaattcttc cctgtctggt ttactggct gtgtgccttt tacggggcgt      2568
196 gcggaattct tccaaaatgg tgagcaaagc tctgttctgg atgccgatta tgtgaccttg      2628
198 tcttccctgg atttcgataa acttcccgat gattgccaaag gacaagaact caaagttcat      2688
200 aacgagctgg ttgatcttct gcctggttct ttgaaatct ccaggacttc tggttcagaa      2748
202 atcttgctga ctagcgatgt cgatgaactc gatcggccag caatccgctt ggtgtcctgg      2808
204 atcgcgccga catcttaagg tgccagggtc ttaaagtgcc aggggttctg tgggatccgt      2868

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206 acactgggttc ccattgacttt gactattgag gaaatcgcca agaccaaaaa gcttttggtt 2928
208 gtgtccgatt ttgatggaac catcgagga ttagcaagg acgcttaca cgttcctatc 2988
210 aaccagaaat ccctcaaggc gg 3010
213 <210> SEQ ID NO: 2
214 <211> LENGTH: 485
215 <212> TYPE: PRT
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218 <400> SEQUENCE: 2
220 Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
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224 Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
225 20 25 30
228 Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
229 35 40 45
232 Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
233 50 55 60
236 Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser
237 65 70 75 80
240 Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
241 85 90 95
244 Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
245 100 105 110
248 His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
249 115 120 125
252 Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
253 130 135 140
256 Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly
257 145 150 155 160
260 Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
261 165 170 175
264 Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val
265 180 185 190
268 Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln
269 195 200 205
272 Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu
273 210 215 220
276 Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu
277 225 230 235 240
280 Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile
281 245 250 255
284 Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu
285 260 265 270
288 Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg
289 275 280 285
292 Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu
293 290 295 300
296 Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln
297 305 310 315 320
300 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg

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301          325          330          335
304 Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg
305          340          345          350
308 Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn
309          355          360          365
312 Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
313          370          375          380
316 Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
317 385          390          395          400
320 Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
321          405          410          415
324 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
325          420          425          430
328 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
329          435          440          445
332 Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
333          450          455          460
336 His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
337 465          470          475          480
340 Ser Gly Glu Asn Ser
341          485
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345 <211> LENGTH: 24
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347 <213> ORGANISM: Corynebacterium glutamicum
349 <400> SEQUENCE: 3
350 cacctattct aaggacttct tcga
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354 <211> LENGTH: 22
355 <212> TYPE: DNA
356 <213> ORGANISM: Corynebacterium glutamicum
358 <400> SEQUENCE: 4
359 accaaccagg tggaatctgt ca

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VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date